



SEQUENCE LISTING

<110> Robert E. Klem

<120> METHODS AND COMPOSITIONS FOR TREATING A
CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF

<130> 10412-022-999

<140> 10/053,645
<141> 2002-01-22

<150> 60/263,244
<151> 2001-01-22

<160> 43

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Oligonucleotide

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Oligonucleotide

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Oligonucleotide

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Oligonucleotide

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Oligonucleotide

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Oligonucleotide

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<210> 14
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Oligonucleotide	
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 1 5 10 15

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 Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
 20 25 30

gga gat gtg ggc gcc gcg ccc ccg ggg gcc ccc gca ccg ggc atc 144
 Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
 35 40 45

ttc tcc tcc cag ccc ggg cac acg ccc cat cca gcc gca tcc cgc gac 192
 Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
 50 55 60

ccg gtc gcc agg acc tcg ccg ctg cag acc ccg gct gcc ccc ggc gcc 240
 Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
 65 70 75 80

gcc gcg ggg cct gcg ctc agc ccg gtg cca cct gtg gtc cac ctg gcc 288
 Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
 85 90 95

ctc cgc caa gcc ggc gac gac ttc tcc cgc cgc tac cgc ggc gac ttc 336
 Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
 100 105 110

gcc gag atg tcc agc cag ctg cac ctg acg ccc ttc acc gcg cgg gga 384
 Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
 115 120 125

cgc ttt gcc acg gtg gtg gag gag ctc ttc agg gac ggg gtg aac tgg 432
 Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
 130 135 140

ggg agg att gtg gcc ttc ttt gag ttc ggt ggg gtc atg tgt gtg gag 480
 Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
 145 150 155 160

agc gtc aac cgg gag atg tcg ccc ctg gtg gac aac atc gcc ctg tgg 528
 Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
 165 170 175

atg act gag tac ctg aac cgg cac ctg cac acc tgg atc cag gat aac 576
 Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
 180 185 190

gga ggc tgg gat gcc ttt gtg gaa ctg tac ggc ccc agc atg cgg cct	624
Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro	
195 200 205	
ctg ttt gat ttc tcc tgg ctg tct ctg aag act ctg ctc agt ttg gcc	672
Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala	
210 215 220	
ctg gtg gga gct tgc atc acc ctg ggt gcc tat ctg agc cac aag	717
Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Ser His Lys	
225 230 235	

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 <213> Homo Sapiens

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 Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
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 Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
 35 40 45
 Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
 50 55 60
 Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
 65 70 75 80
 Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
 85 90 95
 Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
 100 105 110
 Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
 115 120 125
 Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
 130 135 140
 Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
 145 150 155 160
 Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
 165 170 175
 Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
 180 185 190
 Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
 195 200 205
 Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
 210 215 220
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 225 230 235

<210> 22
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 <213> Homo Sapiens

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 aag tac atc cat tat aag ctg tcg cag agg ggc tac gag tgg gat gcg 96
 Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
 20 25 30

 gga gat gtg ggc gcc gcg ccc cc_g ggg gcc gcc ccc gca cc_g ggc atc 144
 Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
 35 40 45

 ttc tcc tcc cag ccc ggg cac acg ccc cat cca gcc gca tcc cgc gac 192
 Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
 50 55 60

 ccg gtc gcc agg acc tcg cc_g ctg cag acc cc_g gct gcc ccc ggc gcc 240
 Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
 65 70 75 80

 gcc gcg ggg cct gcg ctc agc cc_g gtg cca cct gtg gtc cac ctg gcc 288
 Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
 85 90 95

 ctc cgc caa gcc ggc gac gac ttc tcc cgc cgc tac cc_g ggc gac ttc 336
 Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
 100 105 110

 gcc gag atg tcc agc cag ctg cac ctg acg ccc ttc acc gcg cgg gga 384
 Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
 115 120 125

 ccg ttt gcc acg gtg gtg gag gag ctc ttc agg gac ggg gtg aac tgg 432
 Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
 130 135 140

 ggg agg att gtg gcc ttc ttt gag ttc ggt ggg gtc atg tgt gtg gag 480
 Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
 145 150 155 160

 agc gtc aac cgg gag atg tcg ccc ctg gtg gac aac atc gcc ctg tgg 528
 Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
 165 170 175

 atg act gag tac ctg aac cgg cac ctg cac acc tgg atc cag gat aac 576
 Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
 180 185 190

 gga ggc tgg gta ggt gca tct ggt gat gtg agt ctg ggc 615
 Gly Gly Trp Val Gly Ala Ser Gly Asp Val Ser Leu Gly
 195 200 205

<210> 23
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Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
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 Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
 35 40 45
 Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
 50 55 60
 Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
 65 70 75 80
 Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
 85 90 95
 Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
 100 105 110
 Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
 115 120 125
 Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
 130 135 140
 Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
 145 150 155 160
 Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
 165 170 175
 Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
 180 185 190
 Gly Gly Trp Val Gly Ala Ser Gly Asp Val Ser Leu Gly
 195 200 205

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<223> Description of artificial sequence: Synthetic Antisense Oligonucleotide

<400> 24

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18

<210> 25

<211> 18

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<213> Artificial sequence

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<223> Description of artificial sequence: Synthetic Antisense Oligonucleotide

<400> 25

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18

<210> 26

<211> 20

<212> DNA

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<223> Description of artificial sequence: Synthetic Antisense Oligonucleotide

<400> 26

gcgcggcgccc cggggcgccca

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<210> 27
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Oligonucleotide

<400> 27
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<210> 28
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Oligonucleotide

<400> 28
agcggcgccg gcggcagcgc 20

<210> 29
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Oligonucleotide

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gggcgggaa gggcgcccgc 20

<210> 30
<211> 84
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Oligonucleotide

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tttggctttt aaaggccgtt ttgt 84

<210> 31
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Oligonucleotide

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tgacgtt 67

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<400> 36		
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Oligonucleotide

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23

<210> 43
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<220>
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Oligonucleotide

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